

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: CHEN, ZHIJIAN J.
- (ii) TITLE OF INVENTION: A KINASE CAPABLE OF SITE-SPECIFIC PHOSPHORYLATION OF I_KB α
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 - (B) STREET: 1100 NEW YORK AVENUE, SUITE 600
 - (C) CITY: WASHINGTON
 - (D) STATE: DC
 - (E) COUNTRY: US
 - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/825,559
 - (B) FILING DATE: 19-MAR-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/616,499
 - (B) FILING DATE: 19-MAR-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: BROWN, ANNE
 - (B) REGISTRATION NUMBER: 36,463
 - (C) REFERENCE/DOCKET NUMBER: 1448.0240001
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202) 371-2600
 - (B) TELEFAX: (202) 371-2540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTGTGACCTC AGGATATCGA GAGCAACT TCCATT

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTGTGACCTC AGGATATCGA GAGAAATACT TCCAT

35

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /note= "CAN BE LEU OR ILE"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /note= "CAN BE LEU OR ILE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Xaa Tyr Val Glu Xaa Glu Arg
1 5

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /note= "CAN BE LEU OR ILE"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 2
(D) OTHER INFORMATION: /note= "CAN BE GLN OR LYS"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /note= "CAN BE LEU OR ILE"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 8
(D) OTHER INFORMATION: /note= "CAN BE LEU OR ILE"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 9
(D) OTHER INFORMATION: /note= "CAN BE LEU OR ILE"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 11
(D) OTHER INFORMATION: /note= "CAN BE LEU OR ILE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Xaa Xaa Glu Val Xaa Glu Thr Xaa Xaa Ser Xaa Glu Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /note= "CAN BE LEU OR ILE"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 7
(D) OTHER INFORMATION: /note= "CAN BE LEU OR ILE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Xaa Phe Thr Thr Met Glu Xaa Met Arg
1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Thr Tyr His Ala Leu Ser Asn Leu Pro Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGGTGACGAG TGGTGGCCGA AGCAGGGGGA CAGCAAGGGA CGCTCAGGCG GGGACCATGG	60
CGGACGGCGG CTCGGAGCGG GCTGACGGGC GCATCGTCAA GATGGAGGTG GACTACAGCG	120
CCACGGTGGGA TCAGCGCCTA CCCGAGTGTG CGAAGTATGC CAAGGAAGGA AGACTTCAAG	180
AAGTCATTGA AACCCCTCTC TCTCTGGAAA AGCAGACTCG TACTGCTTCC GATATGGTAT	240
CGACATCCCG TATCTTAGTT GCAGTAGTGA AGNTGTGCTA TGAGGCTAAA GAATGGGATT	300
TACTTAATTAA AAAATATTAT TGCTTTTGT CCAAAAGGCG GAGTCAAGTT AAAAACAAAGC	360
TAGTTGACAA AAAATGGATT NAACAGTTGC TGTNACTTAT TGTT	404

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATACCAAGAG GTACCAGGAA GCATTGCATT TGGGTTCTCA GCTGCTGCGG GAGTTGAAAA	60
AGATGGACGA CAAAGCTCTT TTGGTGGAAAG TACAGCTTTT AGAAAGCAA ACATACCATG	120
CCCTGAGCAA CCTGCCGAAA GCCCGAGCTG CCTTAACCTTC TTCTCGAACCC ACAGCAAATG	180
CCATCTACTG CCCCTAAAT TGCAGGCCAC CTTGGACATG CAGTCGGGTA TTATCCATGC	240
AGCAGAAGAG AAGGCTTGAA ACTCGTACTC ATACTTCTAT GAGGCATTAA GGGTATGACT	300
CATCGACAGC CCAAGGCATC ACA	323